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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/724,108	12/01/2003	Hideki Thoda	245694US0CONT	3217
22850	7590	07/16/2007		
OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C. 1940 DUKE STREET ALEXANDRIA, VA 22314			EXAMINER SCHLAPKOHL, WALTER	
			ART UNIT	PAPER NUMBER
			1636	
			NOTIFICATION DATE	DELIVERY MODE
			07/16/2007	ELECTRONIC

**Please find below and/or attached an Office communication concerning this application or proceeding.**

The time period for reply, if any, is set in the attached communication.

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<b>Office Action Summary</b>	<b>Application No.</b> 10/724,108	<b>Applicant(s)</b> THODA ET AL.	
	<b>Examiner</b> Walter Schlapkohl	<b>Art Unit</b> 1636	<i>WAF</i>

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

**Period for Reply**

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

**Status**

- 1) ☒ Responsive to communication(s) filed on 16 April 2007.
- 2a) ☐ This action is **FINAL**.                      2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

**Disposition of Claims**

- 4) ☒ Claim(s) 14-25 is/are pending in the application.
- 4a) Of the above claim(s) \_\_\_\_\_ is/are withdrawn from consideration.
- 5) ☐ Claim(s) \_\_\_\_\_ is/are allowed.
- 6) ☒ Claim(s) 14-25 is/are rejected.
- 7) ☐ Claim(s) \_\_\_\_\_ is/are objected to.
- 8) ☐ Claim(s) \_\_\_\_\_ are subject to restriction and/or election requirement.

**Application Papers**

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on \_\_\_\_\_ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.  
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).  
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

**Priority under 35 U.S.C. § 119**

- 12) ☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☒ All    b) ☐ Some \* c) ☐ None of:
1. ☒ Certified copies of the priority documents have been received.
2. ☐ Certified copies of the priority documents have been received in Application No. \_\_\_\_\_.
3. ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

\* See the attached detailed Office action for a list of the certified copies not received.

**Attachment(s)**

- |  |   |
|--|---|
| 1) <input checked="" type="checkbox"/> Notice of References Cited (PTO-892)                                | 4) <input type="checkbox"/> Interview Summary (PTO-413)<br>Paper No(s)/Mail Date. _____ |
| 2) <input type="checkbox"/> Notice of Draftsperson's Patent Drawing Review (PTO-948)                       | 5) <input type="checkbox"/> Notice of Informal Patent Application                       |
| 3) <input type="checkbox"/> Information Disclosure Statement(s) (PTO/SB/08)<br>Paper No(s)/Mail Date _____ | 6) <input checked="" type="checkbox"/> Other: <u>Exhibit B</u>                          |

Art Unit: 1636

**DETAILED ACTION**

Receipt is acknowledged of the papers filed 4/16/2007 in which claims 14 and 20 were amended. Claims 14-25 are pending and under examination in the instant Office action.

***Continued Examination Under 37 CFR 1.114***

A request for continued examination under 37 CFR 1.114, including the fee set forth in 37 CFR 1.17(e), was filed in this application after final rejection. Since this application is eligible for continued examination under 37 CFR 1.114, and the fee set forth in 37 CFR 1.17(e) has been timely paid, the finality of the previous Office action has been withdrawn pursuant to 37 CFR 1.114. Applicant's submission filed on 4/16/2007 has been entered.

***Specification/Application Data Sheet***

The objection to the specification and to the ADS are hereby WITHDRAWN in view of Applicant's amendment filed 4/16/2007 and submission of a substitute ADS on 2/15/2007.

Art Unit: 1636

***Claim Objections***

Claims 15, 17, 21 and 23 are objected to under 37 CFR 1.75(c), as being of improper dependent form for failing to further limit the subject matter of a previous claim. Applicant is required to cancel the claim(s), or amend the claim(s) to place the claim(s) in proper dependent form, or rewrite the claim(s) in independent form. The indicated claims broaden the scope of the independent claim from which they depend in that the independent claims are limited to either a pyruvate decarboxylase pdcl enzyme and/or a serine protease isp6 enzyme and do not encompass any pyruvate decarboxylase as recited in claims 15 and 21, or any serine protease as recited in claims 17 and 23.

Claims 14 and 20 are objected to because of the following informalities: claims 14 and 20 each recite a list of enzymes wherein carboxypeptidase and zinc protease are listed twice (see, e.g., lines 5-6 of claim 14).

Appropriate correction is required.

Art Unit: 1636

*Claim Rejections - 35 USC § 112*

The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

The rejection of claim 20 under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which Applicant regards as the invention is hereby WITHDRAWN in view of Applicant's amendment.

The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 14-25 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the

Art Unit: 1636

claimed invention. This rejection is maintained for reasons of record.

*Response to Arguments*

Applicant argues that the rejection of the claims under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement is no longer applicable as the claims have been amended to define the genes listed in the Examples on pages 10-21. Applicant further argues that these genes were known in the art as evidenced by the references for the genes in the Examples ("SPC," "SPAC" etc) and as open reading frames from the genome sequence of *S. pombe* reported in the journal *Nature* 415(6874):871-880, 2002. Applicant further argues that the fact that these gene structures were known indicates that the specification and claims satisfy the written description requirement.

Applicant's arguments have been carefully considered and have respectfully been found unpersuasive. Despite the fact that Applicant has amended the claims to define the "genes" listed in the examples present in the specification, the recited claims are still drawn to classes of enzymes which comprise numerous species. For example, among the "genes" listed by Applicant in claim 14 is "aminopeptidase" (see claim 14 at line

Art Unit: 1636

7). As is evidenced by Applicant's own specification, there are at least three different aminopeptidases from *S. pombe* which fall into such an enzyme class: dipeptidyl aminopeptidase, cytoplasmic aminopeptidase and aminopeptidase 1 (see specification at page 12, line 6; and page 16, lines 11-21).

Indeed, a search in PubMed revealed 17 entries under "*S. pombe* aminopeptidase" with different sequences and therefore different biochemical properties (see Exhibit B, attached). Although it is clear that Applicant was in possession of sequence information for at least some of the genes encompassed by the claims, Applicant's reference to the Nature paper by Wood et al (*Nature* 415(6874):871-880, 2002) is not persuasive because this paper was filed after Applicant's claimed priority date.

Finally, the fact that some of the gene sequences encompassed by the claims were known at the time of Applicant's filing is not necessarily sufficient written description support for methods which require that such sequences be deleted in order to achieve increased production of a heterologous protein. In other words, Applicant has still not described a representative set of such sequences in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, was in possession of the claimed genus of sequences and sequence combinations capable of being deleted

Art Unit: 1636

such that production of any heterologous protein production was increased.

### **Claim Rejections - 35 USC § 102**

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless -

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

Claims 14, 16, 20 and 22 are rejected under 35 U.S.C. 102(b) as being anticipated by Egel-Matani et al (US Patent No. 6,110,703; of record). This rejection is maintained for reasons of record.

### **Response to Arguments**

Applicant argues that while Egel-Matani et al describe an *S. cerevisiae* YAP3, there is no disclosure for an *S. pombe* YAP3-type protease and certainly not the specific aspartic protease SPCC1795.09 as described in the specification and listed in the claims.

Applicant's arguments have been carefully considered and have respectfully been found unpersuasive. Egel-Matani et al do



Art Unit: 1636

in fact teach a YAP3 enzyme from *S. pombe* at columns 19-20, claims 1 and 11. With regard to Applicant's argument that Egel-Matani et al do not teach the specific aspartic protease SPCC1795.09 as described in the specification, such an argument is not germane because the instant claims do not recite the use of this specific protease; rather the instant claims encompass the use of any aspartic protease.

Claims 14, 17, 19, 20, 23 and 25 are rejected under 35 U.S.C. 102(b) as being anticipated by Simeon et al (Yeast 11:271-282, 1995; IDS Ref. AW). This rejection is maintained for reasons of record.

#### *Response to Arguments*

Applicant concedes that the Simeon et al publication appears to describe a CPY serine protease. However, Applicant argues that Simeon does not describe the specific serine protease isp6 (SPAC1F8.07) which has a sequence which is different and distinct in structure from that of carboxypeptidase Y.

Applicant's arguments have been carefully considered but have respectfully been found unpersuasive. Applicant's arguments are directed to claims which are limited to the

Art Unit: 1636

specific serine protease isp6; however the instant claims encompass any serine protease (see claims 17 and 23) as well as any carboxypeptidase (see claims 14, 19-20 and 25).

***Claim Rejections - 35 USC § 103***

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

(a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

Art Unit: 1636

Claims 14, 18, 20 and 24 are rejected under 35 U.S.C. 103(a) as being unpatentable over Berka et al (WO 00/42203; of record) in view of Giga-Hama et al (*Biotechnol. Appl. Biochem.* 30:235-244, 1999; of record). This rejection is maintained for reasons of record.

*Response to Arguments*

Applicant argues that this rejection is no longer applicable in light of the amended claims and particularly because these two publications do not describe or suggest the specific genes/enzymes defined in claims 14 and 20.

Applicant's arguments have been carefully considered and have respectfully been found unpersuasive because the instant claims have not been narrowed in scope by amendment with regard to the genus of aminopeptidases encompassed. Therefore claims 14, 18, 20 and 24 remain unpatentable over the Berka et al and Giga-Hama et al references.

Claims 14-15 and 20-21 are rejected under 35 U.S.C. 103(a) as being unpatentable over Rajgarhia et al (US Patent Application Publication 2003/0166179 A1) in view of Giga-Hama et al (*Biotechnol. Appl. Biochem.* 30:235-244, 1999; of record).

Art Unit: 1636

This is a new rejection not necessitated by Applicant's amendment.

Rajgarhia et al teach a method of constructing a yeast host cell which produces a heterologous protein comprising deleting or inactivating at least one host gene including pyruvate decarboxylase (including PDC1 of any number of yeast cells including *Saccharomyces cerevisiae* and *K. thermotolerans*, *K. marxianus*, *C. sonorensis*, etc.) and transforming the host cell with a polynucleotide which encodes the heterologous protein (see entire document, especially page 1, paragraphs [0005]-[0006], page 2, paragraphs [0015] and [0019]-[0020]; page 6, paragraph [0074]; page 8, paragraph [0083]; page 17, Example 6; page 22, Example 18; page 32, paragraphs [0305]-[0311]). In addition, Rajgharia et al teach that yeast cells having the ability to grow in the absence of ethanol and acetate while lacking the ability to produce ethanol can redirect the utilization of pyruvate to produce organic products other than ethanol. Finally, Rajgarhia et al teach that it is desirable to delete the PDC genes in strains to be used for lactic acid production (see page 32, paragraph [0305]) and Rajgarhia et al also teach that cells for lactate production can be transformed with a heterologous lactate dehydrogenase gene (see, e.g., the Abstract). While Rajgarhia et al do not explicitly teach such a

Art Unit: 1636

method wherein the inactivation of the pyruvate decarboxylase results in increased heterologous protein production; such would inherently be the case based upon Applicant's admission in the specification that "deletion or inactivation of part or all of the genome of the host unnecessary or detrimental to production of the heterologous protein by its transformation improves the production efficiency of the heterologous protein" (see instant specification at page 3, lines 24-27 and page 4, line 1).

Rajgarhia et al do not teach such a method for an *S. pombe* host cell.

Giga-Hama et al teach the use of *S. pombe* as a host for expression and production of foreign genes. Giga-Hama et al teach that there are several advantages to the use of *S. pombe* (see entire document, especially page 237, 2<sup>nd</sup> column, first paragraph). First, Giga-Hama teach that the *S. pombe* yeast has many characteristics more in common with higher mammalian cells than with other yeasts which makes this yeast host a good model for higher eukaryotic protein production and yields foreign gene products that are "closer to their natural form" (page 237, 2<sup>nd</sup> column, first-third paragraphs). Second, Giga-Hama et al teach that there are a number of vectors and promoters which result in efficient expression of a heterologous protein (see pages 239-240 and Table 1). Finally, Giga-Hama teach that *S. pombe* is a

Art Unit: 1636

good host for the production of a number of different proteins (see, e.g., page 241, Table 2).

It would have been obvious to combine the teachings of Rajgarhia et al with those of Giga-Hama et al because Rajgarhia et al teach the expression of exogenous proteins in yeast cells for production and collection of the heterologous protein and Giga-Hama teaches that *S. pombe* is a good yeast cell for foreign protein production.

One of ordinary skill in the art would have been motivated to combine the teachings of Rajgarhia et al and Giga-Hama et al because Giga-Hama et al teach that there are advantages of using the *S. pombe* cell, especially in cases where the heterologous gene to be produced is a mammalian protein because the mammalian protein would be "closer to [its] nature form." Moreover, Rajgarhia et al teach that use of a host with reduced pyruvate decarboxylase activity is advantageous when, for example, the host cell is to be used in lactic acid production or in situations wherein the utilization of pyruvate can be redirected toward the production of the organic compound to be produced.

Based upon the teachings of the cited references, the high skill of one of ordinary skill in the art, and absent evidence to the contrary, there would have been a reasonable expectation

Art Unit: 1636

of success to result when combining the teachings of Rajgarhia et al with those of Giga-Hama et al.

### **Conclusion**

No claim is allowed.

Certain papers related to this application may be submitted to the Art Unit 1636 by facsimile transmission. The faxing of such papers must conform with the notices published in the Official Gazette, 1156 OG 61 (November 16, 1993) and 1157 OG 94 (December 28, 1993) (see 37 C.F.R. § 1.6(d)). The official fax telephone number for the Group is (571) 273-8300. Note: If Applicant does submit a paper by fax, the original signed copy should be retained by Applicant or Applicant's representative. NO DUPLICATE COPIES SHOULD BE SUBMITTED so as to avoid the processing of duplicate papers in the Office.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to (571) 272-0547.

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Art Unit: 1636

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Any inquiry concerning rejections or objections in this communication or earlier communications from the examiner should be directed to Walter Schlapkohl whose telephone number is (571) 272-4439. The examiner can normally be reached on Monday through Friday from 8:30 AM to 5:00 PM.



If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Dr. Joseph Woitach can be reached at (571) 272-0739.

Walter A. Schlapkohl, Ph.D.  
Patent Examiner  
Art Unit 1636

July 7, 2007

  
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Items 1 - 17 of 17

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SPBC14C8.03 [Schizosaccharomyces pombe]	

gi|3006161|emb|CAA18421.1|[3006161]

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- ☐ **11:** [CAB08750](#) Reports BLink, Conserved I  
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Autophagy protein 5 (Meiotically up-regulated gene 77 protein)  
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LOCUS CAA91125 389 aa linear PLN 18-APR-2005  
DEFINITION SPAC22G7.01c [Schizosaccharomyces pombe].  
ACCESSION CAA91125  
VERSION CAA91125.1 GI:3859775  
DBSOURCE embl accession [Z54328.1](#)  
KEYWORDS .  
SOURCE Schizosaccharomyces pombe (fission yeast)  
ORGANISM [Schizosaccharomyces pombe](#)  
Eukaryota; Fungi; Dikarya; Ascomycota; Taphrinomycotina;  
Schizosaccharomycetes; Schizosaccharomycetales;  
Schizosaccharomycetaceae; Schizosaccharomyces.  
REFERENCE 1 (residues 1 to 389)  
AUTHORS Wood,V., Gwilliam,R., Rajandream,M.A., Lyne,M., Lyne,R.,  
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Gloux,S., Lelaure,V., Mottier,S., Galibert,F., Aves,S.J., Xiang,Z.,  
Hunt,C., Moore,K., Hurst,S.M., Lucas,M., Rochet,M., Gaillardin,C.,  
Tallada,V.A., Garzon,A., Thode,G., Daga,R.R., Cruzado,L.,  
Jimenez,J., Sanchez,M., del Rey,F., Benito,J., Dominguez,A.,  
Reuelta,J.L., Moreno,S., Armstrong,J., Forsburg,S.L., Cerutti,L.,  
Lowe,T., McCombie,W.R., Paulsen,I., Potashkin,J., Shpakovski,G.V.,  
Ussery,D., Barrell,B.G. and Nurse,P.  
TITLE The genome sequence of Schizosaccharomyces pombe  
JOURNAL Nature 415 (6874), 871-880 (2002)  
PUBMED [11859360](#)  
REMARK Erratum:[Nature 2003 Jan 2;421(6918):94. Cerrutti L [corrected to

Cerutti L]]

REFERENCE 2 (residues 1 to 389)

AUTHORS Badcock, K. and Churcher, C.M.

JOURNAL Unpublished

REFERENCE 3 (residues 1 to 389)

AUTHORS Barrell, B.G., Rajandream, M.A., Walsh, S.V. and Wood, V.

TITLE Direct Submission

JOURNAL Submitted (04-OCT-1995) Schizosaccharomyces pombe chromosome I sequencing project, Sanger Centre, Hinxton Hall, Hinxton, Cambridge CB10 1RQ E-mail: pombe@sanger.ac.uk

COMMENT On Nov 11, 1998 this sequence version replaced gi:1015927.

Notes:

Details of S. pombe sequencing at the Sanger Institute are available on the World Wide Web.

(URL, <http://www.genedb.org/genedb/pombe/index.jsp>) (URL, [http://www.sanger.ac.uk/Projects/S\\_pombe/](http://www.sanger.ac.uk/Projects/S_pombe/))

CDS are numbered using the following system eg SPAC5H10.01c. SP (S. pombe), A (chromosome 1), c5H10 (cosmid name), .01 (first CDS), c (complementary strand). However, clones may have been reorientated since the original submission, therefore the complementary strand notation may be invalid for strand inference.

IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once.

FEATURES

Location/Qualifiers

source 1..389

/organism="Schizosaccharomyces pombe"

/strain="972h-"

/db\_xref="taxon:4896"

/chromosome="I"

/map="IL"

/clone="cosmid c22G7"

Protein 1..389

/EC\_number="3.4.11.9"

/name="SPAC22G7.01c"

Region 1..389

/region\_name="PepP"

/note="Xaa-Pro aminopeptidase [Amino acid transport and metabolism]; COG0006"

/db\_xref="CDD:30356"

Region 8..130

/region\_name="Creatinase\_N"

/note="Creatinase/Prolidase N-terminal domain. This family includes the N-terminal non-catalytic domains from creatinase and prolidase. The exact function of this domain is uncertain; pfam01321"

/db\_xref="CDD:65142"

Region 177..>272

/region\_name="Creatinase\_N"

/note="Creatinase/Prolidase N-terminal domain. This family includes the N-terminal non-catalytic domains from creatinase and prolidase. The exact function of this domain is uncertain; pfam01321"

/db\_xref="CDD:65142"

Region 310..>389

/region\_name="APP"

/note="X-Prolyl Aminopeptidase 2. E.C. 3.4.11.9. Also known as X-Pro aminopeptidase, proline aminopeptidase, aminopeptidase P, and aminoacylproline aminopeptidase; cd01085"

CDS

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/gene="SPAC22G7.01c"  
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Z54328.1:1137..1192,Z54328.1:1278..1367))"  
/note="aminopeptidase (predicted); peptidase family M24;  
similar to S. cerevisiae YLL029W"  
/db_xref="GOA:Q09795"  
/db_xref="UniProtKB/Swiss-Prot:Q09795"
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ORIGIN

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61 etsaalftdg ryfnqasqql denwtlmkqg ftgvptweey ctqmtkcnek vgidsslitf  
121 paakalresl flksgavlv gdhnlvdivw gasrpkeple klivqeikya glgvdeklhn  
181 lreamkeqki eafvvsmlde vawlynlr ga dvpynpvffa yslvtldeaf lyvderkvtp  
241 evskhldgfv kilpydrvfs daknsnltri gissktswci atsfggetkvm pilspisqak  
301 gikndaelkg mkechirdgc alveyfawld eylnsgnkin efdaatkleg frrknnlfmg  
361 lsfetisstg pngavihy sp patgsaiid
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Nucleotide

Protein

Genome

Structure

PMC

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Preview/Index

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Display  Show  Range: from  to  Features: ☒ CDD  

1: CAB62423. Reports SPAC22G7.01c [Sch...[gi:32139912].

BLink, Conserved  
Domains, Links[Comment](#) [Features](#) [Sequence](#)

LOCUS CAB62423 242 aa linear PLN 16-APR-2005

DEFINITION SPAC22G7.01c [Schizosaccharomyces pombe].

ACCESSION CAB62423

VERSION CAB62423.2 GI:32139912

DBSOURCE embl accession [AL133359.1](#)

KEYWORDS

SOURCE Schizosaccharomyces pombe (fission yeast)

ORGANISM [Schizosaccharomyces pombe](#)  
Eukaryota; Fungi; Dikarya; Ascomycota; Taphrinomycotina;  
Schizosaccharomycetes; Schizosaccharomycetales;  
Schizosaccharomycetaceae; Schizosaccharomyces.

REFERENCE 1 (residues 1 to 242)

AUTHORS, Wood, V., Gwilliam, R., Rajandream, M. A., Lyne, M., Lyne, R.,  
Stewart, A., Sgouros, J., Peat, N., Hayles, J., Baker, S., Basham, D.,  
Bowman, S., Brooks, K., Brown, D., Brown, S., Chillingworth, T.,  
Churcher, C., Collins, M., Connor, R., Cronin, A., Davis, P.,  
Feltwell, T., Fraser, A., Gentles, S., Goble, A., Hamlin, N., Harris, D.,  
Hidalgo, J., Hodgson, G., Holroyd, S., Hornsby, T., Howarth, S.,  
Huckle, E. J., Hunt, S., Jagels, K., James, K., Jones, L., Jones, M.,  
Leather, S., McDonald, S., McLean, J., Mooney, P., Moule, S.,  
Mungall, K., Murphy, L., Niblett, D., Odell, C., Oliver, K., O'Neil, S.,  
Pearson, D., Quail, M. A., Rabinowitsch, E., Rutherford, K., Rutter, S.,  
Saunders, D., Seeger, K., Sharp, S., Skelton, J., Simmonds, M.,  
Squares, R., Squares, S., Stevens, K., Taylor, K., Taylor, R. G.,  
Tivey, A., Walsh, S., Warren, T., Whitehead, S., Woodward, J.,  
Volckaert, G., Aert, R., Robben, J., Grymonprez, B., Weltjens, I.,  
Vanstreels, E., Rieger, M., Schafer, M., Muller-Auer, S., Gabel, C.,  
Fuchs, M., Dusterhoft, A., Fritz, C., Holzer, E., Moestl, D.,  
Hilbert, H., Borzym, K., Langer, I., Beck, A., Lehrach, H.,  
Reinhardt, R., Pohl, T. M., Eger, P., Zimmermann, W., Wedler, H.,  
Wambutt, R., Purnelle, B., Goffeau, A., Cadieu, E., Dreano, S.,  
Gloux, S., Lelaure, V., Mottier, S., Galibert, F., Aves, S. J., Xiang, Z.,  
Hunt, C., Moore, K., Hurst, S. M., Lucas, M., Rochet, M., Gaillardin, C.,  
Tallada, V. A., Garzon, A., Thode, G., Daga, R. R., Cruzado, L.,  
Jimenez, J., Sanchez, M., del Rey, F., Benito, J., Dominguez, A.,  
Revuelta, J. L., Moreno, S., Armstrong, J., Forsburg, S. L., Cerutti, L.,  
Lowe, T., McCombie, W. R., Paulsen, I., Potashkin, J., Shpakovski, G. V.,  
Ussery, D., Barrell, B. G. and Nurse, P.

TITLE The genome sequence of Schizosaccharomyces pombe

JOURNAL Nature 415 (6874), 871-880 (2002)

PUBMED [11859360](#)

REMARK Erratum: [Nature 2003 Jan 2;421(6918):94. Cerrutti L [corrected to

Cerutti L]]  
 REFERENCE 2 (residues 1 to 242)  
 AUTHORS McDougall,R.C., Rajandream,M.A., Barrell,B.G., Brown,S. and Harris,D.  
 TITLE Direct Submission  
 JOURNAL Submitted (03-DEC-1999) European Schizosaccharomyces genome sequencing project, Sanger Institute, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: pombe@sanger.ac.uk  
 COMMENT On Jun 21, 2003 this sequence version replaced gi:6562186.  
 Notes:  
 Details of S. pombe sequencing at the Sanger Institute are available on the World Wide Web.  
 (URL, <http://www.genedb.org/genedb/pombe/index.jsp>) (URL, [http://www.sanger.ac.uk/Projects/S\\_pombe/](http://www.sanger.ac.uk/Projects/S_pombe/))  
 CDS are numbered using the following system eg SPAC5H10.01c. SP (S. pombe), A (chromosome 1), c5H10 (cosmid name), .01 (first CDS), c (complementary strand). However, clones may have been reorientated since the original submission, therefore the complementary strand notation may be invalid for strand inference.  
 IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once.

FEATURES Location/Qualifiers  
 source 1..242  
 /organism="Schizosaccharomyces pombe"  
 /strain="972h-"  
 /db\_xref="taxon:4896"  
 /chromosome="I"  
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 Protein 1..242  
 /name="SPAC22G7.01c"  
 Region <1..178  
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 /note="X-Prolyl Aminopeptidase 2. E.C. 3.4.11.9. Also known as X-Pro aminopeptidase, proline aminopeptidase, aminopeptidase P, and aminoacylproline aminopeptidase; cd01085"  
 /db\_xref="CDD:29970"  
 CDS 1..242  
 /gene="SPAC22G7.01c"  
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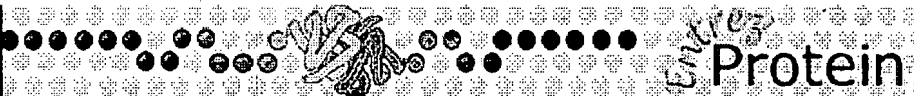
## ORIGIN

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LOCUS CAA90806 513 aa linear PLN 18-APR-2005  
DEFINITION SPAC13A11.05 [Schizosaccharomyces pombe].  
ACCESSION CAA90806  
VERSION CAA90806.1 GI:984226  
DBSOURCE embl accession [Z54096.1](#)  
KEYWORDS .  
SOURCE Schizosaccharomyces pombe (fission yeast)  
ORGANISM [Schizosaccharomyces pombe](#)  
Eukaryota; Fungi; Dikarya; Ascomycota; Taphrinomycotina;  
Schizosaccharomycetes; Schizosaccharomycetales;  
Schizosaccharomycetaceae; Schizosaccharomyces.  
REFERENCE 1 (residues 1 to 513)  
AUTHORS Wood,V., Gwilliam,R., Rajandream,M.A., Lyne,M., Lyne,R.,  
Stewart,A., Sgouros,J., Peat,N., Hayles,J., Baker,S., Basham,D.,  
Bowman,S., Brooks,K., Brown,D., Brown,S., Chillingworth,T.,  
Churcher,C., Collins,M., Connor,R., Cronin,A., Davis,P.,  
Feltwell,T., Fraser,A., Gentles,S., Goble,A., Hamlin,N., Harris,D.,  
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Huckle,E.J., Hunt,S., Jagels,K., James,K., Jones,L., Jones,M.,  
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Reinhardt,R., Pohl,T.M., Eger,P., Zimmermann,W., Wedler,H.,  
Wambutt,R., Purnelle,B., Goffeau,A., Cadieu,E., Dreano,S.,  
Gloux,S., Lelaure,V., Mottier,S., Galibert,F., Aves,S.J., Xiang,Z.,  
Hunt,C., Moore,K., Hurst,S.M., Lucas,M., Rochet,M., Gaillardin,C.,  
Tallada,V.A., Garzon,A., Thode,G., Daga,R.R., Cruzado,L.,  
Jimenez,J., Sanchez,M., del Rey,F., Benito,J., Dominguez,A.,  
Revuelta,J.L., Moreno,S., Armstrong,J., Forsburg,S.L., Cerutti,L.,  
Lowe,T., McCombie,W.R., Paulsen,I., Potashkin,J., Shpakovski,G.V.,  
Ussery,D., Barrell,B.G. and Nurse,P.  
TITLE The genome sequence of Schizosaccharomyces pombe  
JOURNAL Nature 415 (6874), 871-880 (2002)  
PUBMED [11859360](#)  
REMARK Erratum:[Nature 2003 Jan 2;421(6918):94. Cerrutti L [corrected to



Cerutti LJ]  
 REFERENCE 2 (residues 1 to 513)  
 AUTHORS Hunt, S., Devlin, K., Churcher, C.M., Barrell, B.G., Rajandream, M.A. and Walsh, S.V.  
 TITLE Direct Submission  
 JOURNAL Submitted (06-SEP-1995) Schizosaccharomyces pombe chromosome I sequencing project, Sanger Institute, Hinxton Hall, Hinxton, Cambridge CB10 1RQ E-mail: pombe@sanger.ac.uk  
 COMMENT Notes:  
 Details of S. pombe sequencing at the Sanger Institute are available on the World Wide Web.  
 (URL, <http://www.genedb.org/genedb/pombe/index.jsp>) (URL, [http://www.sanger.ac.uk/Projects/S\\_pombe/](http://www.sanger.ac.uk/Projects/S_pombe/))  
 CDS are numbered using the following system eg SPAC5H10.01c. SP (S. pombe), A (chromosome 1), c5H10 (cosmid name), .01 (first CDS), c (complementary strand). However, clones may have been reorientated since the original submission, therefore the complementary strand notation may be invalid for strand inference.  
 IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once.

FEATURES Location/Qualifiers  
 source 1..513  
 /organism="Schizosaccharomyces pombe"  
 /strain="972h-"  
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 Protein 1..513  
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 Region 28..513  
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 /note="Leucyl aminopeptidase [Amino acid transport and metabolism]; COG0260"  
 /db\_xref="CDD:30609"  
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ORIGIN

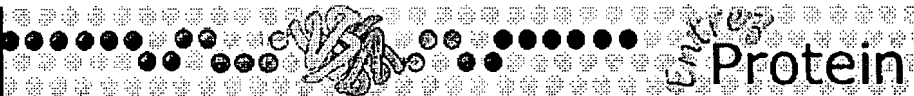
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 121 daalgaalat ydfslrrdhl svyqdekvve kenlftspap erltfqllsn tsekktatae  
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 301 radmgaavm lssiyaleql sipvnavfvt pltenlpsgs aakpgdvifm rnglsveidn

361 tdaegrilila davhyvssqy ktkavieast ltgamlvalg nvftgafvqg eelwknleta  
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LOCUS CAA19013 379 aa linear PLN 16-APR-2005

DEFINITION SPBC3E7.10 [Schizosaccharomyces pombe].

ACCESSION CAA19013

VERSION CAA19013.1 GI:3130036

DBSOURCE embl accession [AL023534.1](#)

KEYWORDS .

SOURCE Schizosaccharomyces pombe (fission yeast)

ORGANISM Schizosaccharomyces pombe  
Eukaryota; Fungi; Dikarya; Ascomycota; Taphrinomycotina;  
Schizosaccharomycetes; Schizosaccharomycetales;  
Schizosaccharomycetaceae; Schizosaccharomyces.

REFERENCE 1 (residues 1 to 379)

AUTHORS Wood,V., Gwilliam,R., Rajandream,M.A., Lyne,M., Lyne,R.,  
Stewart,A., Sgouros,J., Peat,N., Hayles,J., Baker,S., Basham,D.,  
Bowman,S., Brooks,K., Brown,D., Brown,S., Chillingworth,T.,  
Churcher,C., Collins,M., Connor,R., Cronin,A., Davis,P.,  
Feltwell,T., Fraser,A., Gentles,S., Goble,A., Hamlin,N., Harris,D.,  
Hidalgo,J., Hodgson,G., Holroyd,S., Hornsby,T., Howarth,S.,  
Huckle,E.J., Hunt,S., Jagels,K., James,K., Jones,L., Jones,M.,  
Leather,S., McDonald,S., McLean,J., Mooney,P., Moule,S.,  
Mungall,K., Murphy,L., Niblett,D., Odell,C., Oliver,K., O'Neil,S.,  
Pearson,D., Quail,M.A., Rabinowitsch,E., Rutherford,K., Rutter,S.,  
Saunders,D., Seeger,K., Sharp,S., Skelton,J., Simmonds,M.,  
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Vanstreels,E., Rieger,M., Schafer,M., Muller-Auer,S., Gabel,C.,  
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Hunt,C., Moore,K., Hurst,S.M., Lucas,M., Rochet,M., Gaillardin,C.,  
Tallada,V.A., Garzon,A., Thode,G., Daga,R.R., Cruzado,L.,  
Jimenez,J., Sanchez,M., del Rey,F., Benito,J., Dominguez,A.,  
Revuelta,J.L., Moreno,S., Armstrong,J., Forsburg,S.L., Cerutti,L.,  
Lowe,T., McCombie,W.R., Paulsen,I., Potashkin,J., Shpakovski,G.V.,  
Ussery,D., Barrell,B.G. and Nurse,P.

TITLE The genome sequence of Schizosaccharomyces pombe

JOURNAL Nature 415 (6874), 871-880 (2002)

PUBMED [11859360](#)

REMARK Erratum:[Nature 2003 Jan 2;421(6918):94. Cerrutti L [corrected to

Cerutti L]]

REFERENCE 2 (residues 1 to 379)

AUTHORS Lyne,M., Wood,V., Rajandream,M.A., Barrell,B.G., Brown,D. and Churcher,C.M.

TITLE Direct Submission

JOURNAL Submitted (06-MAY-1998) European Schizosaccharomyces genome sequencing project, Sanger Institute, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: pombe@sanger.ac.uk

COMMENT Notes:  
 Details of *S. pombe* sequencing at the Sanger Institute are available on the World Wide Web.  
 (URL, <http://www.genedb.org/genedb/pombe/index.jsp>) (URL, [http://www.sanger.ac.uk/Projects/S\\_pombe/](http://www.sanger.ac.uk/Projects/S_pombe/))  
 CDS are numbered using the following system eg SPAC5H10.01c. SP (*S. pombe*), A (chromosome 1), c5H10 (cosmid name), .01 (first CDS), c (complementary strand). However, clones may have been reorientated since the original submission, therefore the complementary strand notation may be invalid for strand inference.  
 IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once.

FEATURES

	Location/Qualifiers
source	1..379 /organism="Schizosaccharomyces pombe" /strain="972h-" /db_xref="taxon:4896" /chromosome="II" /map="IIR" /clone="cosmid c3E7"
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<u>Region</u>	126..367 /region_name="MetAP1" /note="Methionine Aminopeptidase 1. E.C. 3.4.11.18. Also known as methionyl aminopeptidase and Peptidase M. Catalyzes release of N-terminal amino acids, preferentially methionine, from peptides and arylamides; cd01086" /db_xref="CDD:29971"
<u>CDS</u>	1..379 /gene="SPBC3E7.10" /coded_by="join(AL023534.1:23540..23656, AL023534.1:23709..23729,AL023534.1:23779..23824, AL023534.1:23885..24840)" /note="methionine aminopeptidase (predicted); similar to <i>S. cerevisiae</i> MAP1" /db_xref="GOA:O59730" /db_xref="InterPro:IPR000994" /db_xref="InterPro:IPR001714" /db_xref="InterPro:IPR002467" /db_xref="UniProtKB/Swiss-Prot:O59730"

ORIGIN

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361 tgcevtarl pnsppgplk

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LOCUS CAA94695 486 aa linear PLN 18-APR-2005

DEFINITION SPAC12B10.05 [Schizosaccharomyces pombe].

ACCESSION CAA94695

VERSION CAA94695.1 GI:4008582

DBSOURCE embl accession [Z70721.1](#)

KEYWORDS .

SOURCE Schizosaccharomyces pombe (fission yeast)

ORGANISM [Schizosaccharomyces pombe](#)  
 Eukaryota; Fungi; Dikarya; Ascomycota; Taphrinomycotina;  
 Schizosaccharomycetes; Schizosaccharomycetales;  
 Schizosaccharomycetaceae; Schizosaccharomyces.

REFERENCE 1 (residues 1 to 486)

AUTHORS Wood,V., Gwilliam,R., Rajandream,M.A., Lyne,M., Lyne,R.,  
 Stewart,A., Sgouros,J., Peat,N., Hayles,J., Baker,S., Basham,D.,  
 Bowman,S., Brooks,K., Brown,D., Brown,S., Chillingworth,T.,  
 Churcher,C., Collins,M., Connor,R., Cronin,A., Davis,P.,  
 Feltwell,T., Fraser,A., Gentles,S., Goble,A., Hamlin,N., Harris,D.,  
 Hidalgo,J., Hodgson,G., Holroyd,S., Hornsby,T., Howarth,S.,  
 Huckle,E.J., Hunt,S., Jagels,K., James,K., Jones,L., Jones,M.,  
 Leather,S., McDonald,S., McLean,J., Mooney,P., Moule,S.,  
 Mungall,K., Murphy,L., Niblett,D., Odell,C., Oliver,K., O'Neil,S.,  
 Pearson,D., Quail,M.A., Rabinowitsch,E., Rutherford,K., Rutter,S.,  
 Saunders,D., Seeger,K., Sharp,S., Skelton,J., Simmonds,M.,  
 Squares,R., Squares,S., Stevens,K., Taylor,K., Taylor,R.G.,  
 Tivey,A., Walsh,S., Warren,T., Whitehead,S., Woodward,J.,  
 Volckaert,G., Aert,R., Robben,J., Grymonprez,B., Weltjens,I.,  
 Vanstreels,E., Rieger,M., Schafer,M., Muller-Auer,S., Gabel,C.,  
 Fuchs,M., Dusterhoft,A., Fritz,C., Holzer,E., Moestl,D.,  
 Hilbert,H., Borzym,K., Langer,I., Beck,A., Lehrach,H.,  
 Reinhardt,R., Pohl,T.M., Eger,P., Zimmermann,W., Wedler,H.,  
 Wambutt,R., Purnelle,B., Goffeau,A., Cadieu,E., Dreano,S.,  
 Gloux,S., Lelaure,V., Mottier,S., Galibert,F., Aves,S.J., Xiang,Z.,  
 Hunt,C., Moore,K., Hurst,S.M., Lucas,M., Rochet,M., Gaillardin,C.,  
 Tallada,V.A., Garzon,A., Thode,G., Daga,R.R., Cruzado,L.,  
 Jimenez,J., Sanchez,M., del Rey,F., Benito,J., Dominguez,A.,  
 Revuelta,J.L., Moreno,S., Armstrong,J., Forsburg,S.L., Cerutti,L.,  
 Lowe,T., McCombie,W.R., Paulsen,I., Potashkin,J., Shpakovski,G.V.,  
 Ussery,D., Barrell,B.G. and Nurse,P.

TITLE The genome sequence of Schizosaccharomyces pombe

JOURNAL Nature 415 (6874), 871-880 (2002)

PUBMED [11859360](#)

REMARK Erratum: [Nature 2003 Jan 2;421(6918):94. Cerrutti L [corrected to

Cerutti L]]

REFERENCE 2 (residues 1 to 486)

AUTHORS Badcock, K. and Churcher, C.M.

JOURNAL Unpublished

REFERENCE 3 (residues 1 to 486)

AUTHORS Barrell, B.G., Rajandream, M.A. and Walsh, S.V.

TITLE Direct Submission

JOURNAL Submitted (10-APR-1996) Schizosaccharomyces pombe chromosome I sequencing project, Sanger Institute, Hinxton Hall, Hinxton, Cambridge CB10 1RQ. E-mail: pombe@sanger.ac.uk

COMMENT Notes:

Details of S. pombe sequencing at the Sanger Institute are available on the World Wide Web.

(URL, <http://www.genedb.org/genedb/pombe/index.jsp>) (URL, [http://www.sanger.ac.uk/Projects/S\\_pombe/](http://www.sanger.ac.uk/Projects/S_pombe/))

CDS are numbered using the following system eg SPAC5H10.01c. SP (S. pombe), A (chromosome 1), c5H10 (cosmid name), .01 (first CDS), c (complementary strand). However, clones may have been reorientated since the original submission, therefore the complementary strand notation may be invalid for strand inference.

IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once.

FEATURES

source	Location/Qualifiers
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	/strain="972h-"
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	/chromosome="I"
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	/clone="cosmid c12B10"
<u>Protein</u>	1..486
	/name="SPAC12B10.05"
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	/note="Xaa-Pro aminopeptidase [Amino acid transport and metabolism]; COG0006"
	/db_xref="CDD:30356"
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<u>Region</u>	240..472
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	/db_xref="CDD:29972"
<u>CDS</u>	1..486
	/gene="SPAC12B10.05"
	/coded_by="join(Z70721.1:10068..10239, Z70721.1:10285..10387, Z70721.1:10437..10457, Z70721.1:10497..10523, Z70721.1:10559..10572, Z70721.1:10621..10653, Z70721.1:10697..10824, Z70721.1:10864..11247, Z70721.1:11309..11386,

Z70721.1:11430..11651,Z70721.1:11701..11808,  
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## ORIGIN

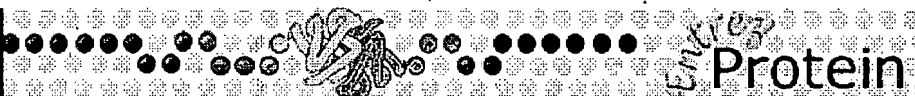
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181 gkksnrifyn yqtgylskmp aasapefiqd tltklfrtst qrsvdellhp lrsikstael  
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361 cctsngwsla dihfesvklm heelkqvgh gtkreitdil yphsigheig leihdcstnn  
421 gyqplrknqv itiepglyvp eedgwpqwaq giairiedsv ivgddkpfvl tsaapkeiee  
481 iealkk

//

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LOCUS CAB11706 467 aa linear PLN 18-APR-2005

DEFINITION SPAC4F10.02 [Schizosaccharomyces pombe].

ACCESSION CAB11706

VERSION CAB11706.1 GI:2388974

DBSOURCE embl accession [Z98980.1](#)

KEYWORDS .

SOURCE Schizosaccharomyces pombe (fission yeast)

ORGANISM [Schizosaccharomyces pombe](#)  
Eukaryota; Fungi; Dikarya; Ascomycota; Taphrinomycotina;  
Schizosaccharomycetes; Schizosaccharomycetales;  
Schizosaccharomycetaceae; Schizosaccharomyces.

REFERENCE 1 (residues 1 to 467)

AUTHORS Wood,V., Gwilliam,R., Rajandream,M.A., Lyne,M., Lyne,R.,  
Stewart,A., Sgouros,J., Peat,N., Hayles,J., Baker,S., Basham,D.,  
Bowman,S., Brooks,K., Brown,D., Brown,S., Chillingworth,T.,  
Churcher,C., Collins,M., Connor,R., Cronin,A., Davis,P.,  
Feltwell,T., Fraser,A., Gentles,S., Goble,A., Hamlin,N., Harris,D.,  
Hidalgo,J., Hodgson,G., Holroyd,S., Hornsby,T., Howarth,S.,  
Huckle,E.J., Hunt,S., Jagels,K., James,K., Jones,L., Jones,M.,  
Leather,S., McDonald,S., McLean,J., Mooney,P., Moule,S.,  
Mungall,K., Murphy,L., Niblett,D., Odell,C., Oliver,K., O'Neil,S.,  
Pearson,D., Quail,M.A., Rabinowitsch,E., Rutherford,K., Rutter,S.,  
Saunders,D., Seeger,K., Sharp,S., Skelton,J., Simmonds,M.,  
Squares,R., Squares,S., Stevens,K., Taylor,K., Taylor,R.G.,  
Tivey,A., Walsh,S., Warren,T., Whitehead,S., Woodward,J.,  
Volckaert,G., Aert,R., Robben,J., Grymonprez,B., Weltjens,I.,  
Vanstreels,E., Rieger,M., Schafer,M., Muller-Auer,S., Gabel,C.,  
Fuchs,M., Dusterhoft,A., Fritz,C., Holzer,E., Moestl,D.,  
Hilbert,H., Borzym,K., Langer,I., Beck,A., Lehrach,H.,  
Reinhardt,R., Pohl,T.M., Eger,P., Zimmermann,W., Wedler,H.,  
Wambutt,R., Purnelle,B., Goffeau,A., Cadieu,E., Dreano,S.,  
Gloux,S., Lelaure,V., Mottier,S., Galibert,F., Aves,S.J., Xiang,Z.,  
Hunt,C., Moore,K., Hurst,S.M., Lucas,M., Rochet,M., Gaillardin,C.,  
Tallada,V.A., Garzon,A., Thode,G., Daga,R.R., Cruzado,L.,  
Jimenez,J., Sanchez,M., del Rey,F., Benito,J., Dominguez,A.,  
Revuelta,J.L., Moreno,S., Armstrong,J., Forsburg,S.L., Cerutti,L.,  
Lowe,T., McCombie,W.R., Paulsen,I., Potashkin,J., Shpakovski,G.V.,  
Ussery,D., Barrell,B.G. and Nurse,P.

TITLE The genome sequence of Schizosaccharomyces pombe

JOURNAL Nature 415 (6874), 871-880 (2002)

PUBMED [11859360](#)

REMARK Erratum:[Nature 2003 Jan 2;421(6918):94. Cerrutti L [corrected to

Cerutti LJ]  
REFERENCE 2 (residues 1 to 467)  
AUTHORS Connor,R., Churcher,C.M., Barrell,B.G., Rajandream,M.A. and Wood,V.  
TITLE Direct Submission  
JOURNAL Submitted (06-SEP-1997) Schizosaccharomyces pombe chromosome I  
sequencing project, Sanger Institute, Hinxton Hall, Hinxton,  
Cambridge CB10 1RQ E-mail: pombe@sanger.ac.uk

COMMENT Notes:  
Details of S. pombe sequencing at the Sanger Institute are  
available on the World Wide Web.  
(URL, <http://www.genedb.org/genedb/pombe/index.jsp>) (URL,  
[http://www.sanger.ac.uk/Projects/S\\_pombe/](http://www.sanger.ac.uk/Projects/S_pombe/))  
CDS are numbered using the following system eg SPAC5H10.01c. SP (S.  
pombe), A (chromosome 1), c5H10 (cosmid name), .01 (first CDS), c  
(complementary strand). However, clones may have been reorientated  
since the original submission, therefore the complementary strand  
notation may be invalid for strand inference.  
IMPORTANT: This sequence MAY NOT be the entire insert of the  
sequenced clone. It may be shorter because we only sequence  
overlapping sections once.

FEATURES Location/Qualifiers  
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Region 15..453  
/region\_name="Peptidase\_M18"  
/note="Aminopeptidase I zinc metalloprotease (M18);  
pfam02127"  
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CDS 1..467  
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cerevisiae APE1"  
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121 twfdrdlsla grvmveeedg rviqynvhid rpllrptla ihldpsanss fsfnmetefv  
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1: CAB58971. Reports SPBC1921.05 [Schizosaccharomyces pombe]

BLink, Conserved

Domains, Links

Comment Features Sequence

LOCUS CAB58971 882 aa linear PLN 16-APR-2005

DEFINITION SPBC1921.05 [Schizosaccharomyces pombe].

ACCESSION CAB58971

VERSION CAB58971.1 GI:6090559

DBSOURCE embl accession AL122033.1

KEYWORDS:

SOURCE Schizosaccharomyces pombe (fission yeast).

ORGANISM Schizosaccharomyces pombe

Eukaryota; Fungi; Dikarya; Ascomycota; Taphrinomycotina;  
Schizosaccharomycetes; Schizosaccharomycetales;  
Schizosaccharomycetaceae; Schizosaccharomyces.

REFERENCE 1 (residues 1 to 882)

AUTHORS Wood,V., Gwilliam,R., Rajandream,M.A., Lyne,M., Lyne,R.,  
Stewart,A., Sgouros,J., Peat,N., Hayles,J., Baker,S., Basham,D.,  
Bowman,S., Brooks,K., Brown,D., Brown,S., Chillingworth,T.,  
Churcher,C., Collins,M., Connor,R., Cronin,A., Davis,P.,  
Feltwell,T., Fraser,A., Gentles,S., Goble,A., Hamlin,N., Harris,D.,  
Hidalgo,J., Hodgson,G., Holroyd,S., Hornsby,T., Howarth,S.,  
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Leather,S., McDonald,S., McLean,J., Mooney,P., Moule,S.,  
Mungall,K., Murphy,L., Niblett,D., Odell,C., Oliver,K., O'Neil,S.,  
Pearson,D., Quail,M.A., Rabinowitsch,E., Rutherford,K., Rutter,S.,  
Saunders,D., Seeger,K., Sharp,S., Skelton,J., Simmonds,M.,  
Squares,R., Squares,S., Stevens,K., Taylor,K., Taylor,R.G.,  
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Volckaert,G., Aert,R., Robben,J., Grymonprez,B., Weltjens,I.,  
Vanstreels,E., Rieger,M., Schafer,M., Muller-Auer,S., Gabel,C.,  
Fuchs,M., Dusterhoft,A., Fritzc,C., Holzer,E., Moestl,D.,  
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Gloux,S., Lelaure,V., Mottier,S., Galibert,F., Aves,S.J., Xiang,Z.,  
Hunt,C., Moore,K., Hurst,S.M., Lucas,M., Rochet,M., Gaillardin,C.,  
Tallada,V.A., Garzon,A., Thode,G., Daga,R.R., Cruzado,L.,  
Jimenez,J., Sanchez,M., del Rey,F., Benito,J., Dominguez,A.,  
Revuelta,J.L., Moreno,S., Armstrong,J., Forsburg,S.L., Cerutti,L.,  
Lowe,T., McCombie,W.R., Paulsen,I., Potashkin,J., Shpakovski,G.V.,  
Ussery,D., Barrell,B.G. and Nurse,P.

TITLE The genome sequence of Schizosaccharomyces pombe

JOURNAL Nature 415 (6874), 871-880 (2002)

PUBMED 11859360

REMARK Erratum: [Nature 2003 Jan 2;421(6918):94. Cerrutti L [corrected to

Cerutti L]]  
 REFERENCE 2 (residues 1 to 882)  
 AUTHORS Seeger, K., Harris, D., McDougall, R.C., Rajandream, M.A. and Barrell, B.G.  
 TITLE Direct Submission  
 JOURNAL Submitted (18-OCT-1999) European Schizosaccharomyces genome sequencing project, Sanger Institute, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: pombe@sanger.ac.uk and  
 COMMENT Notes:  
 Details of *S. pombe* sequencing at the Sanger Institute are available on the World Wide Web.  
 (URL, <http://www.genedb.org/genedb/pombe/index.jsp>) (URL, [http://www.sanger.ac.uk/Projects/S\\_pombe/](http://www.sanger.ac.uk/Projects/S_pombe/))  
 CDS are numbered using the following system eg SPAC5H10.01c. SP (*S. pombe*), A (chromosome 1), c5H10 (cosmid name), .01 (first CDS), c (complementary strand). However, clones may have been reorientated since the original submission, therefore the complementary strand notation may be invalid for strand inference.  
 IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once.

FEATURES Location/Qualifiers  
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## ORIGIN

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241 eqgkfaaalg aktldffsgv fgepylplkc dmvaipdfea gamenwglvt yrllaailvse
301 dsaatvierv aevvqhelah qwfgnlvtmq fwdglwlneg fatwmswfs nhfypewkvw
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481 lieqhrflst gdvkpeedtv iywaplklkt mkdgkavvde kavlsdrskk ikvdkeales
541 yklnseqsgl yrvnysadh1 kklsqiavek pdylsveda gliadvasls ragygvkst
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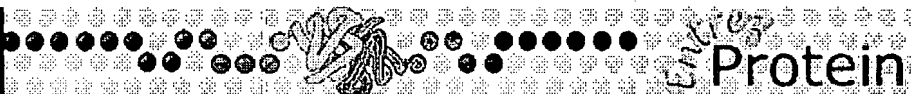
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LOCUS CAA21804 1019 aa linear PLN 16-APR-2005

DEFINITION SPBP8B7.19 [Schizosaccharomyces pombe].

ACCESSION CAA21804

VERSION CAA21804.1 GI:3810843

DBSOURCE embl accession [AL032684.1](#)

KEYWORDS .

SOURCE Schizosaccharomyces pombe (fission yeast)

ORGANISM [Schizosaccharomyces pombe](#)  
Eukaryota; Fungi; Dikarya; Ascomycota; Taphrinomycotina;  
Schizosaccharomycetes; Schizosaccharomycetales;  
Schizosaccharomycetaceae; Schizosaccharomyces.

REFERENCE 1 (residues 1 to 1019)

AUTHORS Wood,V., Gwilliam,R., Rajandream,M.A., Lyne,M., Lyne,R.,  
Stewart,A., Sgouros,J., Peat,N., Hayles,J., Baker,S., Basham,D.,  
Bowman,S., Brooks,K., Brown,D., Brown,S., Chillingworth,T.,  
Churcher,C., Collins,M., Connor,R., Cronin,A., Davis,P.,  
Feltwell,T., Fraser,A., Gentles,S., Goble,A., Hamlin,N., Harris,D.,  
Hidalgo,J., Hodgson,G., Holroyd,S., Hornsby,T., Howarth,S.,  
Huckle,E.J., Hunt,S., Jagels,K., James,K., Jones,L., Jones,M.,  
Leather,S., McDonald,S., McLean,J., Mooney,P., Moule,S.,  
Mungall,K., Murphy,L., Niblett,D., Odell,C., Oliver,K., O'Neil,S.,  
Pearson,D., Quail,M.A., Rabinowitsch,E., Rutherford,K., Rutter,S.,  
Saunders,D., Seeger,K., Sharp,S., Skelton,J., Simmonds,M.,  
Squares,R., Squares,S., Stevens,K., Taylor,K., Taylor,R.G.,  
Tivey,A., Walsh,S., Warren,T., Whitehead,S., Woodward,J.,  
Volckaert,G., Aert,R., Robben,J., Grymonprez,B., Weltjens,I.,  
Vanstreels,E., Rieger,M., Schafer,M., Muller-Auer,S., Gabel,C.,  
Fuchs,M., Dusterhoft,A., Fritz,C., Holzer,E., Moestl,D.,  
Hilbert,H., Borzym,K., Langer,I., Beck,A., Lehrach,H.,  
Reinhardt,R., Pohl,T.M., Eger,P., Zimmermann,W., Wedler,H.,  
Wambutt,R., Purnelle,B., Goffeau,A., Cadieu,E., Dreano,S.,  
Gloux,S., Lelaure,V., Mottier,S., Galibert,F., Aves,S.J., Xiang,Z.,  
Hunt,C., Moore,K., Hurst,S.M., Lucas,M., Rochet,M., Gaillardin,C.,  
Tallada,V.A., Garzon,A., Thode,G., Daga,R.R., Cruzado,L.,  
Jimenez,J., Sanchez,M., del Rey,F., Benito,J., Dominguez,A.,  
Revuelta,J.L., Moreno,S., Armstrong,J., Forsburg,S.L., Cerutti,L.,  
Lowe,T., McCombie,W.R., Paulsen,I., Potashkin,J., Shpakovski,G.V.,  
Ussery,D., Barrell,B.G. and Nurse,P.

TITLE The genome sequence of Schizosaccharomyces pombe

JOURNAL Nature 415 (6874), 871-880 (2002)

PUBMED [11859360](#)

REMARK Erratum:[Nature 2003 Jan 2;421(6918):94. Cerrutti L [corrected to

Cerutti L]]

REFERENCE 2 (residues 1 to 1019)

AUTHORS Beck,A., Reinhardt,R., Lyne,M., Rajandream,M.A. and Barrell,B.G.

TITLE Direct Submission

JOURNAL Submitted (29-OCT-1998) European Schizosaccharomyces genome sequencing project, Sanger Institute, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: pombe@sanger.ac.uk and Max Planck Institut fuer Molekulare Genetik, Ihnestr. 73, D-14195 Berlin, Germany

COMMENT Notes:  
 Details of S. pombe sequencing at the Sanger Institute are available on the World Wide Web.  
 (URL, <http://www.genedb.org/genedb/pombe/index.jsp>) (URL, [http://www.sanger.ac.uk/Projects/S\\_pombe/](http://www.sanger.ac.uk/Projects/S_pombe/))  
 CDS are numbered using the following system eg SPAC5H10.01c. SP (S. pombe), A (chromosome 1), c5H10 (cosmid name), .01 (first CDS), c (complementary strand). However, clones may have been reorientated since the original submission, therefore the complementary strand notation may be invalid for strand inference.  
 IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once.

FEATURES

	Location/Qualifiers
source	1..1019 /organism="Schizosaccharomyces pombe" /strain="972h-" /db_xref="taxon:4896" /chromosome="II" /map="IIR" /clone="p1 p8B7"
<u>Protein</u>	1..1019 /name="SPBP8B7.19"
<u>Region</u>	1..935 /region_name="COG5406" /note="Nucleosome binding factor SPN, SPT16 subunit [Transcription / DNA replication, recombination, and repair / Chromatin structure and dynamics]; COG5406" /db_xref="CDD:34965"
<u>Region</u>	181..427 /region_name="CDC68-like" /note="Related to aminopeptidase P and aminopeptidase M, a member of this domain family is present in cell division control protein 68, a transcription factor; cd01091" /db_xref="CDD:29976"
<u>Region</u>	540..690 /region_name="SPT16" /note="FACT complex subunit (SPT16/CDC68). Proteins in this family are subunits the FACT complex. The FACT complex plays a role in transcription initiation and promotes binding of TATA-binding protein (TBP) to a TATA box in chromatin; pfam08644" /db_xref="CDD:72069"
<u>Region</u>	838..>920 /region_name="Rtt106" /note="Histone chaperone Rtt106-like. This family includes Rtt106, a histone chaperone involved in heterochromatin-mediated silencing; pfam08512" /db_xref="CDD:71940"
<u>CDS</u>	1..1019 /gene="SPBP8B7.19"



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 involved in chromatin mediated transcriptional regulation  
 (predicted); involved in cell cycle control (predicted);  
 global transcription factor C; similar to S. cerevisiae  
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ORIGIN

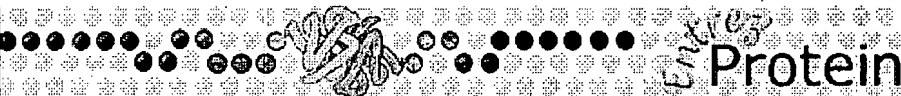
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LOCUS CAA18421 426 aa linear PLN 16-APR-2005

DEFINITION SPBC14C8.03 [Schizosaccharomyces pombe].

ACCESSION CAA18421

VERSION CAA18421.1 GI:3006161

DBSOURCE embl accession [AL022305.1](#)

KEYWORDS .

SOURCE Schizosaccharomyces pombe (fission yeast)

ORGANISM [Schizosaccharomyces pombe](#)  
Eukaryota; Fungi; Dikarya; Ascomycota; Taphrinomycotina;  
Schizosaccharomycetes; Schizosaccharomycetales;  
Schizosaccharomycetaceae; Schizosaccharomyces.

REFERENCE 1 (residues 1 to 426)

AUTHORS Wood,V., Gwilliam,R., Rajandream,M.A., Lyne,M., Lyne,R.,  
Stewart,A., Sgouros,J., Peat,N., Hayles,J., Baker,S., Basham,D.,  
Bowman,S., Brooks,K., Brown,D., Brown,S., Chillingworth,T.,  
Churcher,C., Collins,M., Connor,R., Cronin,A., Davis,P.,  
Feltwell,T., Fraser,A., Gentles,S., Goble,A., Hamlin,N., Harris,D.,  
Hidalgo,J., Hodgson,G., Holroyd,S., Hornsby,T., Howarth,S.,  
Huckle,E.J., Hunt,S., Jagels,K., James,K., Jones,L., Jones,M.,  
Leather,S., McDonald,S., McLean,J., Mooney,P., Moule,S.,  
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Hunt,C., Moore,K., Hurst,S.M., Lucas,M., Rochet,M., Gaillardin,C.,  
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Ussery,D., Barrell,B.G. and Nurse,P.

TITLE The genome sequence of Schizosaccharomyces pombe

JOURNAL Nature 415 (6874), 871-880 (2002)

PUBMED [11859360](#)

REMARK Erratum: [Nature 2003 Jan 2;421(6918):94. Cerrutti L [corrected to

Cerutti L]]

REFERENCE 2 (residues 1 to 426)

AUTHORS Lyne,M., Rajandream,M.A., Barrell,B.G. and Volckaert,G.

TITLE Direct Submission

JOURNAL Submitted (27-MAR-1998) European Schizosaccharomyces genome sequencing project, Sanger Institute, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: pombe@sanger.ac.uk and Katholieke Universiteit Leuven, Faculty of Agricultural and Applied Biological Sciences, Laboratory of Gene Technology, Kardinaal Mercierlaan 92 Blok F, B-3001 Leuven, Belgium

COMMENT Notes:  
 Details of S. pombe sequencing at the Sanger Institute are available on the World Wide Web.  
 (URL, <http://www.genedb.org/genedb/pombe/index.jsp>) (URL, [http://www.sanger.ac.uk/Projects/S\\_pombe/](http://www.sanger.ac.uk/Projects/S_pombe/))  
 CDS are numbered using the following system eg SPAC5H10.01c. SP (S. pombe), A (chromosome 1), c5H10 (cosmid name), .01 (first CDS), c (complementary strand). However, clones may have been reorientated since the original submission, therefore the complementary strand notation may be invalid for strand inference.  
 IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once.

FEATURES

source	Location/Qualifiers
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	/strain="972h-"
	/db_xref="taxon:4896"
	/chromosome="II"
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<u>Protein</u>	1..426
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	/db_xref="CDD:29973"
<u>CDS</u>	1..426
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ORIGIN

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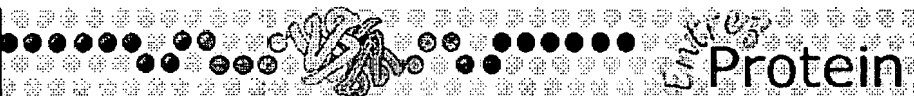
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//

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LOCUS CAB45933 451 aa linear PLN 20-JUN-2003

DEFINITION SPBC18A7.01 [Schizosaccharomyces pombe].

ACCESSION CAB45933

VERSION CAB45933.1 GI:5263087

DBSOURCE embl accession [AL080287.1](#)

KEYWORDS

SOURCE Schizosaccharomyces pombe (fission yeast)

ORGANISM [Schizosaccharomyces pombe](#)  
Eukaryota; Fungi; Dikarya; Ascomycota; Taphrinomycotina;  
Schizosaccharomycetes; Schizosaccharomycetales;  
Schizosaccharomycetaceae; Schizosaccharomyces.

REFERENCE 1 (residues 1 to 451)

AUTHORS Wood,V., Gwilliam,R., Rajandream,M.A., Lyne,M., Lyne,R.,  
Stewart,A., Sgouros,J., Peat,N., Hayles,J., Baker,S., Basham,D.,  
Bowman,S., Brooks,K., Brown,D., Brown,S., Chillingworth,T.,  
Churcher,C., Collins,M., Connor,R., Cronin,A., Davis,P.,  
Feltwell,T., Fraser,A., Gentles,S., Goble,A., Hamlin,N., Harris,D.,  
Hidalgo,J., Hodgson,G., Holroyd,S., Hornsby,T., Howarth,S.,  
Huckle,E.J., Hunt,S., Jagels,K., James,K., Jones,L., Jones,M.,  
Leather,S., McDonald,S., McLean,J., Mooney,P., Moule,S.,  
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Pearson,D., Quail,M.A., Rabinowitsch,E., Rutherford,K., Rutter,S.,  
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Hunt,C., Moore,K., Hurst,S.M., Lucas,M., Rochet,M., Gaillardin,C.,  
Tallada,V.A., Garzon,A., Thode,G., Daga,R.R., Cruzado,L.,  
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Revuelta,J.L., Moreno,S., Armstrong,J., Forsburg,S.L., Cerutti,L.,  
Lowe,T., McCombie,W.R., Paulsen,I., Potashkin,J., Shpakovski,G.V.,  
Ussery,D., Barrell,B.G. and Nurse,P.

TITLE The genome sequence of Schizosaccharomyces pombe

JOURNAL Nature 415 (6874), 871-880 (2002)

PUBMED [11859360](#)

REMARK Erratum: [Nature 2003 Jan 2;421(6918):94. Cerrutti L [corrected to

Cerutti L]]

REFERENCE 2 (residues 1 to 451)

AUTHORS Wood, V., Rajandream, M.A., Barrell, B.G. and Moreno, S.

TITLE Direct Submission

JOURNAL Submitted (25-JUN-1999) European Schizosaccharomyces genome sequencing project, Sanger Institute, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: pombe@sanger.ac.uk and Instituto de Microbiologia Bioquímica, CSIC Universidad de Salamanca, Edificio Departamental, Campus Miguel de Unamuno, 37007 Salamanca, Spain

COMMENT Notes:  
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 (URL, <http://www.genedb.org/genedb/pombe/index.jsp>) (URL, [http://www.sanger.ac.uk/Projects/S\\_pombe/](http://www.sanger.ac.uk/Projects/S_pombe/))  
 CDS are numbered using the following system eg SPAC5H10.01c. SP (*S. pombe*), A (chromosome 1), c5H10 (cosmid name), .01 (first CDS), c (complementary strand). However, clones may have been reorientated since the original submission, therefore the complementary strand notation may be invalid for strand inference.  
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FEATURES

source	Location/Qualifiers
	1..451
	/organism="Schizosaccharomyces pombe"
	/strain="972h-"
	/db_xref="taxon:4896"
	/chromosome="II"
	/map="IIR"
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<u>Protein</u>	1..451
	/name="SPBC18A7.01"
<u>Region</u>	227..432
	/region_name="APP-like"
	/note="Similar to Prolidase and Aminopeptidase P. The members of this subfamily presumably catalyse hydrolysis of Xaa-Pro dipeptides and/or release of any N-terminal amino acid, including proline, that is linked with proline; cd01092"
	/db_xref="CDD:29977"
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	/gene="SPBC18A7.01"
	/coded_by="AL080287.1:892..2247"
	/note="aminopeptidase (predicted); dipeptidase (predicted); metalloproteinase; peptidase family M24; no apparent <i>S. cerevisiae</i> ortholog"
	/db_xref="GOA:Q9UUD8"
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ORIGIN

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421 deigirieda vlasdvpill tnfrakspye p

//

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Genome

Structure

PMC

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Features:

☒ CDD☐ 1: [CAB08750](#). Reports SPAC3A12.05c [Sch...[gi:14422268][BLink](#), [Conserved](#)[Domains](#), [Links](#)[Comment](#) [Features](#) [Sequence](#)

LOCUS CAB08750 1174 aa linear PLN 18-APR-2005

DEFINITION SPAC3A12.05c [Schizosaccharomyces pombe].

ACCESSION CAB08750

VERSION CAB08750.2 GI:14422268

DBSOURCE embl accession [Z95395.1](#)

KEYWORDS .

SOURCE Schizosaccharomyces pombe (fission yeast)

ORGANISM [Schizosaccharomyces pombe](#)  
 Eukaryota; Fungi; Dikarya; Ascomycota; Taphrinomycotina;  
 Schizosaccharomycetes; Schizosaccharomycetales;  
 Schizosaccharomycetaceae; Schizosaccharomyces.

REFERENCE 1 (residues 1 to 1174)

AUTHORS Wood,V., Gwilliam,R., Rajandream,M.A., Lyne,M., Lyne,R.,  
 Stewart,A., Sgouros,J., Peat,N., Hayles,J., Baker,S., Basham,D.,  
 Bowman,S., Brooks,K., Brown,D., Brown,S., Chillingworth,T.,  
 Churcher,C., Collins,M., Connor,R., Cronin,A., Davis,P.,  
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 Hilbert,H., Borzym,K., Langer,I., Beck,A., Lehrach,H.,  
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 Hunt,C., Moore,K., Hurst,S.M., Lucas,M., Rochet,M., Gaillardin,C.,  
 Tallada,V.A., Garzon,A., Thode,G., Daga,R.R., Cruzado,L.,  
 Jimenez,J., Sanchez,M., del Rey,F., Benito,J., Dominguez,A.,  
 Revuelta,J.L., Moreno,S., Armstrong,J., Forsburg,S.L., Cerutti,L.,  
 Lowe,T., McCombie,W.R., Paulsen,I., Potashkin,J., Shpakovski,G.V.,  
 Ussery,D., Barrell,B.G. and Nurse,P.

TITLE The genome sequence of Schizosaccharomyces pombe

JOURNAL Nature 415 (6874), 871-880 (2002)

PUBMED [11859360](#)

REMARK Erratum: [Nature 2003 Jan 2;421(6918):94. Cerrutti L [corrected to



Cerutti L]]

REFERENCE 2 (residues 1 to 1174)

AUTHORS Badcock, K. and Churcher, C.M.

JOURNAL Unpublished

REFERENCE 3 (residues 1 to 1174)

AUTHORS Wood, V., Barrell, B.G. and Rajandream, M.A.

TITLE Direct Submission

JOURNAL Submitted (01-MAY-1997) Schizosaccharomyces pombe chromosome I sequencing project, Sanger Institute, Hinxton Hall, Hinxton, Cambridge CB10 1RQ E-mail: pombe@sanger.ac.uk

COMMENT On Jun 13, 2001 this sequence version replaced gi:2104421.

Notes:

Details of S. pombe sequencing at the Sanger Institute are available on the World Wide Web.

(URL, <http://www.genedb.org/genedb/pombe/index.jsp>) (URL, [http://www.sanger.ac.uk/Projects/S\\_pombe/](http://www.sanger.ac.uk/Projects/S_pombe/))

CDS are numbered using the following system eg SPAC5H10.01c. SP (S. pombe), A (chromosome 1), c5H10 (cosmid name), .01 (first CDS), c (complementary strand). However, clones may have been reorientated since the original submission, therefore the complementary strand notation may be invalid for strand inference.

IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once.

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301 saiditgyyl pkyaeevent cvflykamdf fvreygsypf nsfklcfvde tnfpfiistps
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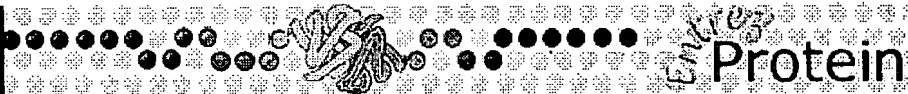
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LOCUS CAB11208 743 aa linear PLN 18-APR-2005

DEFINITION SPAC14C4.15c [Schizosaccharomyces pombe].

ACCESSION CAB11208

VERSION CAB11208.1 GI:2330688

DBSOURCE embl accession [Z98596.1](#)

KEYWORDS .

SOURCE Schizosaccharomyces pombe (fission yeast)

ORGANISM [Schizosaccharomyces pombe](#)  
Eukaryota; Fungi; Dikarya; Ascomycota; Taphrinomycotina;  
Schizosaccharomycetes; Schizosaccharomycetales;  
Schizosaccharomycetaceae; Schizosaccharomyces.

REFERENCE 1 (residues 1 to 743)

AUTHORS Wood,V., Gwilliam,R., Rajandream,M.A., Lyne,M., Lyne,R.,  
Stewart,A., Sgouros,J., Peat,N., Hayles,J., Baker,S., Basham,D.,  
Bowman,S., Brooks,K., Brown,D., Brown,S., Chillingworth,T.,  
Churcher,C., Collins,M., Connor,R., Cronin,A., Davis,P.,  
Feltwell,T., Fraser,A., Gentles,S., Goble,A., Hamlin,N., Harris,D.,  
Hidalgo,J., Hodgson,G., Holroyd,S., Hornsby,T., Howarth,S.,  
Huckle,E.J., Hunt,S., Jagels,K., James,K., Jones,L., Jones,M.,  
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Pearson,D., Quail,M.A., Rabbintowitsch,E., Rutherford,K., Rutter,S.,  
Saunders,D., Seeger,K., Sharp,S., Skelton,J., Simmonds,M.,  
Squares,R., Squares,S., Stevens,K., Taylor,K., Taylor,R.G.,  
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Gloux,S., Lelaure,V., Mottier,S., Galibert,F., Aves,S.J., Xiang,Z.,  
Hunt,C., Moore,K., Hurst,S.M., Lucas,M., Rochet,M., Gaillardin,C.,  
Tallada,V.A., Garzon,A., Thode,G., Daga,R.R., Cruzado,L.,  
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Lowe,T., McCombie,W.R., Paulsen,I., Potashkin,J., Shpakovski,G.V.,  
Ussery,D., Barrell,B.G. and Nurse,P.

TITLE The genome sequence of Schizosaccharomyces pombe

JOURNAL Nature 415 (6874), 871-880 (2002)

PUBMED [11859360](#)

REMARK Erratum: [Nature 2003 Jan 2;421(6918):94. Cerrutti L [corrected to

Cerutti L]]  
 REFERENCE 2 (residues 1 to 743)  
 AUTHORS Devlin,K., Churcher,C.M., Barrell,B.G., Rajandream,M.A. and Wood,V.  
 TITLE Direct Submission  
 JOURNAL Submitted (14-AUG-1997) Schizosaccharomyces pombe chromosome I  
 sequencing project, Sanger Institute, Wellcome Trust Genome Campus,  
 Hinxton, Cambridge CB10 1SA E-mail: pombe@sanger.ac.uk  
 COMMENT Notes:  
 Details of S. pombe sequencing at the Sanger Institute are  
 available on the World Wide Web.  
 (URL, <http://www.genedb.org/genedb/pombe/index.jsp>) (URL,  
[http://www.sanger.ac.uk/Projects/S\\_pombe/](http://www.sanger.ac.uk/Projects/S_pombe/))  
 CDS are numbered using the following system eg SPAC5H10.01c. SP (S.  
 pombe), A (chromosome 1), c5H10 (cosmid name), .01 (first CDS), c  
 (complementary strand). However, clones may have been reorientated  
 since the original submission, therefore the complementary strand  
 notation may be invalid for strand inference.  
 IMPORTANT: This sequence MAY NOT be the entire insert of the  
 sequenced clone. It may be shorter because we only sequence  
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☐ 1: [CAA20739](#). Reports SPBC18A7.01 [Schizosaccharomyces pombe][BLink](#), [Conserved Domains](#), [Links](#)[Comment](#) [Features](#) [Sequence](#)

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DEFINITION SPBC18A7.01 [Schizosaccharomyces pombe].  
ACCESSION CAA20739  
VERSION CAA20739.2 GI:6782390  
DBSOURCE embl accession [AL031534.1](#)  
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SOURCE Schizosaccharomyces pombe (fission yeast)  
ORGANISM [Schizosaccharomyces pombe](#)  
Eukaryota; Fungi; Dikarya; Ascomycota; Taphrinomycotina;  
Schizosaccharomycetes; Schizosaccharomycetales;  
Schizosaccharomycetaceae; Schizosaccharomyces.  
REFERENCE 1 (residues 1 to 243)  
AUTHORS Wood,V., Gwilliam,R., Rajandream,M.A., Lyne,M., Lyne,R.,  
Stewart,A., Sgouros,J., Peat,N., Hayles,J., Baker,S., Basham,D.,  
Bowman,S., Brooks,K., Brown,D., Brown,S., Chillingworth,T.,  
Churcher,C., Collins,M., Connor,R., Cronin,A., Davis,P.,  
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Huckle,E.J., Hunt,S., Jagels,K., James,K., Jones,L., Jones,M.,  
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Pearson,D., Quail,M.A., Rabinowitsch,E., Rutherford,K., Rutter,S.,  
Saunders,D., Seeger,K., Sharp,S., Skelton,J., Simmonds,M.,  
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Lowe,T., McCombie,W.R., Paulsen,I., Potashkin,J., Shpakovski,G.V.,  
Ussery,D., Barrell,B.G. and Nurse,P.  
TITLE The genome sequence of Schizosaccharomyces pombe  
JOURNAL Nature 415 (6874), 871-880 (2002)  
PUBMED [11859360](#)  
REMARK Erratum: [Nature 2003 Jan 2;421(6918):94. Cerrutti L [corrected to

Cerutti L]]  
 REFERENCE 2 (residues 1 to 243)  
 AUTHORS Gwilliam,R., Rajandream,M.A., Barrell,B.G., Skelton,J. and Churcher,C.M.  
 TITLE Direct Submission  
 JOURNAL Submitted (07-SEP-1998) European Schizosaccharomyces genome sequencing project, Sanger Institute, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: pombe@sanger.ac.uk  
 COMMENT On Jan 27, 2000 this sequence version replaced gi:3560152.  
 Notes:  
 Details of S. pombe sequencing at the Sanger Institute are available on the World Wide Web.  
 (URL, <http://www.genedb.org/genedb/pombe/index.jsp>) (URL, [http://www.sanger.ac.uk/Projects/S\\_pombe/](http://www.sanger.ac.uk/Projects/S_pombe/))  
 CDS are numbered using the following system eg SPAC5H10.01c. SP (S. pombe), A (chromosome 1), c5H10 (cosmid name), .01 (first CDS), c (complementary strand). However, clones may have been reorientated since the original submission, therefore the complementary strand notation may be invalid for strand inference.  
 IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once.

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[Comment](#) [Features](#) [Sequence](#)

LOCUS CAA22858 612 aa linear PLN 16-APR-2005  
 DEFINITION SPCC1322.05c [Schizosaccharomyces pombe].  
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 VERSION CAA22858.1 GI:4176545  
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 Eukaryota; Fungi; Dikarya; Ascomycota; Taphrinomycotina;  
 Schizosaccharomycetes; Schizosaccharomycetales;  
 Schizosaccharomycetaceae; Schizosaccharomyces.  
 REFERENCE 1 (residues 1 to 612)  
 AUTHORS Wood,V., Gwilliam,R., Rajandream,M.A., Lyne,M., Lyne,R.,  
 Stewart,A., Sgouros,J., Peat,N., Hayles,J., Baker,S., Basham,D.,  
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 Lowe,T., McCombie,W.R., Paulsen,I., Potashkin,J., Shpakovski,G.V.,  
 Ussery,D., Barrell,B.G. and Nurse,P.  
 TITLE The genome sequence of Schizosaccharomyces pombe  
 JOURNAL Nature 415 (6874), 871-880 (2002)  
 PUBMED 11859360  
 REMARK Erratum: [Nature 2003 Jan 2;421(6918):94. Cerrutti L [corrected to



6

Cerutti L]]

REFERENCE 2 (residues 1 to 612)

AUTHORS Lucas,M., Gaillardin,C., Lyne,M., Rajandream,M.A. and Barrell,B.G.

TITLE Direct Submission

JOURNAL Submitted (20-JAN-1999) European Schizosaccharomyces genome sequencing project, Sanger Institute, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: pombe@sanger.ac.uk and INRA - CBAI, Laboratoire de Genetique Moleculaire et Cellulaire, Route de Thiverval, F-78850 Thiverval Grignon, France

COMMENT Notes:  
 Details of *S. pombe* sequencing at the Sanger Institute are available on the World Wide Web.  
 (URL, <http://www.genedb.org/genedb/pombe/index.jsp>) (URL, [http://www.sanger.ac.uk/Projects/S\\_pombe/](http://www.sanger.ac.uk/Projects/S_pombe/))  
 CDS are numbered using the following system eg SPAC5H10.01c. SP (*S. pombe*), A (chromosome 1), c5H10 (cosmid name), .01 (first CDS), c (complementary strand). However, clones may have been reorientated since the original submission, therefore the complementary strand notation may be invalid for strand inference.  
 IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once.

FEATURES

	Location/Qualifiers
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<u>Region</u>	464..608 /region_name="Leuk-A4-hydro_C" /note="Leukotriene A4 hydrolase, C-terminal; pfam09127" /db_xref="CDD:72544"
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ORIGIN

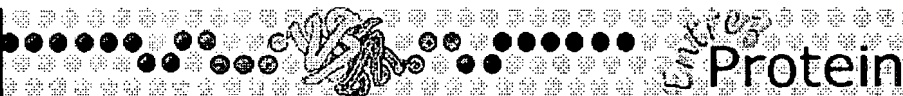
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481 knsddpskfs skdienwsag qkslfdvvy eavsfphnyi krmgdvysfa esknaelsfr  
541 ffklalksky kplyntiaer vgsvglrmkfv rpifrlnea drafaietfe kykhfyhkic  
601 asqvekdgl se

//

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LOCUS CAA20138 793 aa linear PLN 16-APR-2005

DEFINITION SPACUNK4.08 [Schizosaccharomyces pombe].

ACCESSION CAA20138

VERSION CAA20138.1 GI:3395554

DBSOURCE embl accession [AL031180.3](#)

KEYWORDS .

SOURCE Schizosaccharomyces pombe (fission yeast)

ORGANISM [Schizosaccharomyces pombe](#)  
Eukaryota; Fungi; Dikarya; Ascomycota; Taphrinomycotina;  
Schizosaccharomycetes; Schizosaccharomycetales;  
Schizosaccharomycetaceae; Schizosaccharomyces.

REFERENCE 1 (residues 1 to 793)

AUTHORS Wood,V., Gwilliam,R., Rajandream,M.A., Lyne,M., Lyne,R.,  
Stewart,A., Sgouros,J., Peat,N., Hayles,J., Baker,S., Basham,D.,  
Bowman,S., Brooks,K., Brown,D., Brown,S., Chillingworth,T.,  
Churcher,C., Collins,M., Connor,R., Cronin,A., Davis,P.,  
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Hidalgo,J., Hodgson,G., Holroyd,S., Hornsby,T., Howarth,S.,  
Huckle,E.J., Hunt,S., Jagels,K., James,K., Jones,L., Jones,M.,  
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Mungall,K., Murphy,L., Niblett,D., Odell,C., Oliver,K., O'Neil,S.,  
Pearson,D., Quail,M.A., Rabinowitsch,E., Rutherford,K., Rutter,S.,  
Saunders,D., Seeger,K., Sharp,S., Skelton,J., Simmonds,M.,  
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Tivey,A., Walsh,S., Warren,T., Whitehead,S., Woodward,J.,  
Volckaert,G., Aert,R., Robben,J., Grymonprez,B., Weltjens,I.,  
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Fuchs,M., Dusterhoft,A., Fritz,C., Holzer,E., Moestl,D.,  
Hilbert,H., Borzym,K., Langer,I., Beck,A., Lehrach,H.,  
Reinhardt,R., Pohl,T.M., Eger,P., Zimmermann,W., Wedler,H.,  
Wambutt,R., Purnelle,B., Goffeau,A., Cadieu,E., Dreano,S.,  
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Hunt,C., Moore,K., Hurst,S.M., Lucas,M., Rochet,M., Gaillardin,C.,  
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Jimenez,J., Sanchez,M., del Rey,F., Benito,J., Dominguez,A.,  
Revuelta,J.L., Moreno,S., Armstrong,J., Forsburg,S.L., Cerutti,L.,  
Lowe,T., McCombie,W.R., Paulsen,I., Potashkin,J., Shpakovski,G.V.,  
Ussery,D., Barrell,B.G. and Nurse,P.

TITLE The genome sequence of Schizosaccharomyces pombe

JOURNAL Nature 415 (6874), 871-880 (2002)

PUBMED [11859360](#)

REMARK Erratum: [Nature 2003 Jan 2;421(6918):94. Cerrutti L [corrected to

Cerutti L]]

COMMENT Notes:  
 Details of *S. pombe* sequencing at the Sanger Institute are available on the World Wide Web.  
 (URL, <http://www.genedb.org/genedb/pombe/index.jsp>) (URL, [http://www.sanger.ac.uk/Projects/S\\_pombe/](http://www.sanger.ac.uk/Projects/S_pombe/))  
 CDS are numbered using the following system eg SPAC5H10.01c. SP (*S. pombe*), A (chromosome 1), c5H10 (cosmid name), .01 (first CDS), c (complementary strand). However, clones may have been reorientated since the original submission, therefore the complementary strand notation may be invalid for strand inference.  
 IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once.

FEATURES Location/Qualifiers

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//

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Display  Show  Send to Range: from  to  Features: ☒ CDD  ☐ 1: [CAA19290](#). Reports SPBC4B4.10c [Schizosaccharomyces pombe] [gi:3169097]BLink, Conserved  
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LOCUS CAA19290 261 aa linear PLN 16-APR-2005

DEFINITION SPBC4B4.10c [Schizosaccharomyces pombe].

ACCESSION CAA19290

VERSION CAA19290.1 GI:3169097

DBSOURCE embl accession [AL023706.1](#)

KEYWORDS .

SOURCE Schizosaccharomyces pombe (fission yeast)

ORGANISM [Schizosaccharomyces pombe](#)  
Eukaryota; Fungi; Dikarya; Ascomycota; Taphrinomycotina;  
Schizosaccharomycetes; Schizosaccharomycetales;  
Schizosaccharomycetaceae; Schizosaccharomyces.

REFERENCE 1 (residues 1 to 261)

AUTHORS Wood,V., Gwilliam,R., Rajandream,M.A., Lyne,M., Lyne,R.,  
Stewart,A., Sgouros,J., Peat,N., Hayles,J., Baker,S., Basham,D.,  
Bowman,S., Brooks,K., Brown,D., Brown,S., Chillingworth,T.,  
Churcher,C., Collins,M., Connor,R., Cronin,A., Davis,P.,  
Feltwell,T., Fraser,A., Gentles,S., Goble,A., Hamlin,N., Harris,D.,  
Hidalgo,J., Hodgson,G., Holroyd,S., Hornsby,T., Howarth,S.,  
Huckle,E.J., Hunt,S., Jagels,K., James,K., Jones,L., Jones,M.,  
Leather,S., McDonald,S., McLean,J., Mooney,P., Moule,S.,  
Mungall,K., Murphy,L., Niblett,D., Odell,C., Oliver,K., O'Neil,S.,  
Pearson,D., Quail,M.A., Rabinowitsch,E., Rutherford,K., Rutter,S.,  
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Reinhardt,R., Pohl,T.M., Eger,P., Zimmermann,W., Wedler,H.,  
Wambutt,R., Purnelle,B., Goffeau,A., Cadieu,E., Dreano,S.,  
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Tallada,V.A., Garzon,A., Thode,G., Daga,R.R., Cruzado,L.,  
Jimenez,J., Sanchez,M., del Rey,F., Benito,J., Dominguez,A.,  
Revuelta,J.L., Moreno,S., Armstrong,J., Forsburg,S.L., Cerutti,L.,  
Lowe,T., McCombie,W.R., Paulsen,I., Potashkin,J., Shpakovski,G.V.,  
Ussery,D., Barrell,B.G. and Nurse,P.

TITLE The genome sequence of Schizosaccharomyces pombe

JOURNAL Nature 415 (6874), 871-880 (2002)

PUBMED [11859360](#)

REMARK Erratum: [Nature 2003 Jan 2;421(6918):94. Cerrutti L [corrected to

Cerutti L]]  
 REFERENCE 2 (residues 1 to 261)  
 AUTHORS Beck,A., Reinhardt,R., Lyne,M., Wood,V., Rajandream,M.A. and Barrell,B.G.  
 TITLE Direct Submission  
 JOURNAL Submitted (27-MAY-1997) European Schizosaccharomyces genome sequencing project, Sanger Institute, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: pombe@sanger.ac.uk and Max Planck Institut fuer Molekulare Genetik, Ihnestr. 73, D-14195 Berlin, Germany  
 COMMENT Notes:  
 Details of S. pombe sequencing at the Sanger Institute are available on the World Wide Web.  
 (URL, <http://www.genedb.org/genedb/pombe/index.jsp>) (URL, [http://www.sanger.ac.uk/Projects/S\\_pombe/](http://www.sanger.ac.uk/Projects/S_pombe/))  
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 IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once.  
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 //

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☐ 1: [O74971](#). Reports Autophagy protein...[gi:62899674]

[BLink](#), [Conserved Domains](#), [Links](#)

Comment Features Sequence

**LOCUS** O74971 261 aa linear PLN 26-JUN-2007  
**DEFINITION** Autophagy protein 5 (Meiotically up-regulated gene 77 protein).  
**ACCESSION** O74971  
**VERSION** O74971 GI:62899674  
**DBSOURCE** swissprot: locus ATG5\_SCHPO, accession [O74971](#);  
class: standard.  
created: Apr 26, 2005.  
sequence updated: Nov 1, 1998.  
annotation updated: Jun 26, 2007.  
xrefs: [AL023706.1](#), [CAA19290.1](#), [T40482](#)  
xrefs (non-sequence databases): GeneDB\_Spombe:SPBC4B4.10c,  
ArrayExpress:O74971, GO:0005829, GO:0005634, GO:0030437,  
InterPro:IPR007239, PANTHER:PTHR13040, Pfam:PF04106  
**KEYWORDS** Autophagy; Complete proteome; Meiosis; Nucleus; Protein transport;  
Transport; Ubl conjugation.  
**SOURCE** Schizosaccharomyces pombe (fission yeast)  
**ORGANISM** Schizosaccharomyces pombe  
Eukaryota; Fungi; Dikarya; Ascomycota; Taphrinomycotina;  
Schizosaccharomycetes; Schizosaccharomycetales;  
Schizosaccharomycetaceae; Schizosaccharomyces.  
**REFERENCE** 1 (residues 1 to 261)  
**AUTHORS** Wood,V., Gwilliam,R., Rajandream,M.A., Lyne,M., Lyne,R.,  
Stewart,A., Sgouros,J., Peat,N., Hayles,J., Baker,S., Basham,D.,  
Bowman,S., Brooks,K., Brown,D., Brown,S., Chillingworth,T.,  
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Hunt,C., Moore,K., Hurst,S.M., Lucas,M., Rochet,M., Gaillardin,C.,

Tallada,V.A., Garzon,A., Thode,G., Daga,R.R., Cruzado,L., Jimenez,J., Sanchez,M., del Rey,F., Benito,J., Dominguez,A., Revuelta,J.L., Moreno,S., Armstrong,J., Forsburg,S.L., Cerutti,L., Lowe,T., McCombie,W.R., Paulsen,I., Potashkin,J., Shpakovski,G.V., Ussery,D., Barrell,B.G. and Nurse,P.

TITLE The genome sequence of *Schizosaccharomyces pombe*  
JOURNAL Nature 415 (6874), 871-880 (2002)  
PUBMED 11859360  
REMARK NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
STRAIN=ATCC 38366 / 972  
Erratum:[Nature 2003 Jan 2;421(6918):94. Cerrutti L [corrected to Cerutti L]]

REFERENCE 2 (residues 1 to 261)  
AUTHORS Martin-Castellanos,C., Blanco,M., Rozalen,A.E., Perez-Hidalgo,L., Garcia,A.I., Conde,F., Mata,J., Ellermeier,C., Davis,L., San-Segundo,P., Smith,G.R. and Moreno,S.

TITLE A large-scale screen in *S. pombe* identifies seven novel genes required for critical meiotic events  
JOURNAL Curr. Biol. 15 (22), 2056-2062 (2005)  
PUBMED 16303567  
REMARK FUNCTION.

REFERENCE 3 (residues 1 to 261)  
AUTHORS Matsuyama,A., Arai,R., Yashiroda,Y., Shirai,A., Kamata,A., Sekido,S., Kobayashi,Y., Hashimoto,A., Hamamoto,M., Hiraoka,Y., Horinouchi,S. and Yoshida,M.

TITLE ORFeome cloning and global analysis of protein localization in the fission yeast *Schizosaccharomyces pombe*  
JOURNAL Nat. Biotechnol. 24 (7), 841-847 (2006)  
PUBMED 16823372  
REMARK SUBCELLULAR LOCATION [LARGE SCALE ANALYSIS].  
Erratum:[Nat Biotechnol. 2006 Aug;24(8):1033]

COMMENT On Apr 26, 2005 this sequence version replaced gi:7490112.  
[FUNCTION] Involved in cytoplasm to vacuole transport (Cvt) and autophagy vesicles formation. May be required for atg8 association to the vesicle membranes (By similarity). Has a role in meiosis.  
[SUBCELLULAR LOCATION] Cytoplasm. Nucleus. Membrane; peripheral membrane protein (By similarity).  
[PTM] Conjugated to atg12; which is essential for autophagy (By similarity).  
[SIMILARITY] Belongs to the ATG5 family.

FEATURES  
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Region 73..261

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for the import of aminopeptidase I via the  
cytoplasm-to-vacuole targeting pathway; pfam04106"  
/db_xref="CDD:67711"  
bond(148)  
/gene="atg5"  
/locus_tag="SPBC4B4.10c"  
/bond_type="xlink"  
/inference="non-experimental evidence, no additional  
details recorded"  
/note="Glycyl lysine isopeptide (Lys-Gly) (interchain with  
G-Cter in ATG12) (By similarity)."
```

ORIGIN

```
1 mnvdnnkgni pellwngtis vridyegns1 aylanvprqs yfaqilpnavq rllapsipls  
61 ecwldyngvp lkwhwpvgll fdlltvfdpd tprapvlwri qlrsglfptt kilqmetmdt  
121 frtyffnclk esdyvrngss sgiialskae tdywnailn hdydfrpia ikilfskskf  
181 iplkiylgan apiiqtsapl gsslgeflnk rlpdlfpdcd kflivkpvih gitiflqsvl  
241 delnrdfcyi dgflhivlmk v
```

//

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Jun 19 2007 13:56:00